

SEQUENCE LISTING

<110> Rittershaus, Charles W.
Thomas, Lawrence J.
Avant Immunotherapeutics, Inc.

<120> Xenogeneic Cholesteryl Ester Transfer Protein (CETP)
for Modulation of CETP Activity

<130> TCS-420.1 PCT seqlist

<140> PCT/US98/22145

<141> 1998-10-20

<150> 08/954,643

<151> 1997-10-20

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 476

<212> PRT

<213> Homo sapiens

<300>

<301> Drayna, Dennis

<302> Cloning and Sequencing of Human Cholesteryl Ester
Transfer cDNA

<303> Nature

<304> 327

<306> 632-634

<307> 1987-06-18

<313> 1 TO 476

<400> 1

Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val Cys Arg Ile Thr
1 5 10 15

Lys Pro Ala Leu Leu Val Leu Asn His Glu Thr Ala Lys Val Ile Gln
20 25 30

Thr Ala Phe Gln Arg Ala Ser Tyr Pro Asp Ile Thr Gly Glu Lys Ala
35 40 45

Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile
50 55 60

Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu Ala Lys
 65 70 75 80
 Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr
 85 90 95
 Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Trp Leu Gly Ile Asp Gln Ser
 100 105 110
 Ile Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln
 115 120 125
 Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys Tyr
 130 135 140
 Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro
 145 150 155 160
 Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys
 165 170 175
 Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Val Ile Ser Asn
 180 185 190
 Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
 195 200 205
 Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr
 210 215 220
 Ala Ser Tyr Leu Glu Ser His His Lys Gly His Phe Ile Tyr Lys Asn
 225 230 235 240
 Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Thr Leu Leu Gly
 245 250 255
 Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser
 260 265 270
 Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser Leu Met
 275 280 285
 Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr Asn
 290 295 300
 Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln
 305 310 315 320

Val Thr Val His Cys Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys
 325 330 335
 Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro Arg
 340 345 350
 Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp Ile Val
 355 360 365
 Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu
 370 375 380
 Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu Ser
 385 390 395 400
 Ser Ser Glu Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
 405 410 415
 Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe Thr Ala Leu
 420 425 430
 Met Asn Ser Lys Gly Val Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile
 435 440 445
 Ile Thr Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe Pro
 450 455 460
 Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
 465 470 475

<210> 2

<211> 1428

<212> DNA

<213> Homo sapiens

<300>

<301> Drayna, Dennis

 <302> Cloning and Sequencing of Human Cholesteryl Ester
 Transfer cDNA

<303> Nature

<304> 327

<306> 632-634

<307> 1987-06-18

<313> 1 TO 476

<400> 2

tgctccaaag gcacctcgca cgaggcaggc atcgtgtgcc gcatcaccaa gctgcccctc 60
 ctggtgttga accacgagac tgccaaggtg atccagaccg ccttcagcg agccagctac 120
 ccagatatca cggcgagagaa ggccatgatg ctccctggcc aagtcaagta tgggttgac 180
 aacatccaga tcagccactt gtccatcgcc agcagccagg tggagctggt ggaagccaag 240
 tccattgatg tctccattca gaacgtgtct gtggtcttca aggggaccct gaagtatggc 300
 tacaccactg cctggtggct ggggtattgat cagtccattg acttcgagat cgactctgcc 360
 attgacctcc agatcaacac acagctgacc tgtgactctg gtagagtgcg gaccgatgcc 420
 cctgactgct acctgtcttt ccataagctg ctccctgcac tccaagggga gcgagagcct 480
 ggggtggatca agcagctggt cacaatttc atctccttca ccctgaagct ggtcctgaag 540
 ggacagatct gcaaagagat caacgtcatc tctaactca tggccgattt tgtccagaca 600
 agggctgcca gcatcctttc agatggagac attgggggtg acatttccct gacaggtgat 660
 cccgtcatca cagcctccta cctggagtcc catcacaagg gtcatttcat ctacaagaat 720
 gtctcagagg acctccccct cccaccttc tcgcccacac tgctggggga ctcccgcag 780
 ctgtacttct ggttctctga gcgagtcttc cactcgtgg ccaaggtagc tttccaggat 840
 ggccgcctca tgctcagcct gatgggagac gaggttcaagg cagtgtgga gacctggggc 900
 ttcaacacca accaggaaat cttccaagag gttgtcggcg gcttccccag ccaggcccaa 960
 gtcaccgtcc actgcctcaa gatgcccaag atctcctgcc aaaacaaggg agtcgtggtc 1020
 aattcttcag tgatggtgaa attcctcttt ccacgcccag accagcaaca ttctgtagct 1080
 tacacatttg aagaggatat cgtgactacc gtccaggcct cctattctaa gaaaaagctc 1140
 ttcttaagcc tcttgattt ccagattaca ccaaagactg tttccaactt gactgagagc 1200
 agtcccgagt ccatccagag cttcctgcag tcaatgatca ccgctgtggg catccctgag 1260
 gtcatgtctc ggctcgaggt agtgtttaca gccctcatga acagcaaagg cgtgagcctc 1320
 ttcgacatca tcaaccctga gattatcact cgagatggct tctgctgct gcagatggac 1380
 tttggcttcc ctgagcacct gctggtggat ttcctccaga gcttgagc 1428

<210> 3

<211> 496

<212> PRT

<213> *Oryctolagus cuniculus*

<300>

<301> Nagashima, Mariko

 <302> Cloning and mRNA tissue distribution of rabbit
 cholesteryl ester transfer protein

<303> J. Lipid Res.

<304> 29

<306> 1643-1649

<307> 1988

<313> 1 TO 496

<400> 3

Cys	Pro	Lys	Gly	Ala	Ser	Tyr	Glu	Ala	Gly	Ile	Val	Cys	Arg	Ile	Thr
1				5					10				15		

Lys	Pro	Ala	Leu	Leu	Val	Leu	Asn	Gln	Glu	Thr	Ala	Lys	Val	Val	Gln
			20					25					30		

Thr	Ala	Phe	Gln	Arg	Ala	Gly	Tyr	Pro	Asp	Val	Ser	Gly	Glu	Arg	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35 40 45

Val Met Leu Leu Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile
50 55 60

Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp Ala Lys
65 70 75 80

Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr
85 90 95

Leu Asn Tyr Ser Tyr Thr Ser Ala Trp Gly Leu Gly Ile Asn Gln Ser
100 105 110

Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu
115 120 125

Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys Tyr
130 135 140

Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro
145 150 155 160

Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys
165 170 175

Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser Asn
180 185 190

Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
195 200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr
210 215 220

Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys Asn
225 230 235 240

Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu Gly
245 250 255

Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser
260 265 270

Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu Thr
275 280 285

Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr Asn

290 295 300
 Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala
 305 310 315 320
 Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn
 325 330 335
 Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe Pro
 340 345 350
 Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp Ile
 355 360 365
 Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His
 370 375 380
 Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser Ser
 385 390 395 400
 Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
 405 410 415
 Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser Leu
 420 425 430
 Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Ala
 435 440 445
 Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile Ile
 450 455 460
 Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp
 465 470 475 480
 Phe Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
 485 490 495

<210> 4

<211> 1488

<212> DNA

<213> *Oryctolagus cuniculus*

<300>

<301> Nagashima, Mariko
 <302> Cloning and mRNA tissue distribution of rabbit
 cholesteryl ester transfer protein
 <303> J. Lipid Res.
 <304> 29
 <306> 1643-1649
 <307> 1988
 <313> 1 TO 496

<400> 4
 tgtcccaaag gcgcctccta cgaggctggc atcgtgtgtc gcatcaccaa gcccgccctc 60
 ttgggtgtga accaagagac ggccaaggtg gtccagacgg ccttccagcg cgccggctat 120
 ccggacgtca gcggcgagag ggccgtgatg ctccctggcc ggggtcaagta cgggctgcac 180
 aacctccaga tcagccacct gtccatcgcc agcagccagg tggagctggt ggacgccaaag 240
 accatcgacg tcgccatcca gaacgtgtcc gtggtcttca aggggaccct gaactacagc 300
 tacacgagtg cctgggggtt gggcatcaat cagtctgtcg acttcgagat cgactctgcc 360
 attgacctcc agatcaacac agagctgacc tgcgacgctg gcagtgtgcg caccaatgcc 420
 cccgactgct acctggcttt ccataaactg ctccctgcacc tccaggggga gcgcgagccg 480
 ggggtggctca agcagctctt cacaaacttc atctccttca ccctgaagct gattctgaag 540
 cgacaggtct gcaatgagat caacaccatc tccaacatca tggctgactt tgtccagacg 600
 agggccgcca gcatcctctc agatggagac atcgggggtg acatttccgt gacggggggc 660
 cctgtcatca cagccaccta cctggagtcc catcacaagg gtcacttcac gcacaagaac 720
 gtctccgagg ccttccccct cgcgccttc cgcgccgtc ttctggggga ctcccgcatg 780
 ctctacttct ggttctccga tcaagtgtc aactccctgg ccaggggcgc cttccaggag 840
 ggccgtctcg tgctcagcct gacaggggat gaggttcaaga aagtgtgga gaccaggggt 900
 ttgcacacca accaggaaat cttccaggag ctttccagag gccttccac cggccaggcc 960
 caggtagccg tccactgcct taagtgccc aagatctct gccagaaccg ggggtgtcgtg 1020
 gtgtcttctt ccgtcgccgt gacgttccgc ttccccgc cagatggccg agaagctgtg 1080
 gcctacaggt ttgaggagga tatcatcacc accgtccagg cctctactc ccagaaaaag 1140
 ctcttcttac acctcttga tttccagtgc gtgccggcca gcggaagggc aggcagctca 1200
 gcaaattctt ccgtggccct caggactgag gctaaggctg tttccaacct gactgagagc 1260
 cgctccgagt ccctgcagag ctctctccgc tccctgatcg ccacgggtgg catcccgag 1320
 gtcagtgttc ggctcgaggt ggcgttcaca gccctcatga acagcaaagg cctggacctc 1380
 ttcgaaatca tcaacccga gattatcact ctcgatgggt gcctgctgct gcagatggac 1440
 ttcggttttc ccaagcacct gctggtggat ttctgcaga gcctgagc 1488

<210> 5
 <211> 477
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: humanized
 rabbit CETP protein

<400> 5
 Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys Arg Ile Thr
 1 5 10 15

Lys Pro Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Val Gln
20 25 30

Thr Ala Phe Gln Arg Ala Gly Tyr Pro Asp Val Ser Gly Glu Arg Ala
35 40 45

Val Met Leu Leu Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile
50 55 60

Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp Ala Lys
65 70 75 80

Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr
85 90 95

Leu Asn Tyr Ser Tyr Thr Ser Ala Trp Gly Leu Gly Ile Asn Gln Ser
100 105 110

Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu
115 120 125

Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys Tyr
130 135 140

Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro
145 150 155 160

Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys
165 170 175

Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser Asn
180 185 190

Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
195 200 205

Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr
210 215 220

Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys Asn
225 230 235 240

Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu Gly
245 250 255

Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser
260 265 270

Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu Thr
 275 280 285

Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr Asn
 290 295 300

Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala
 305 310 315 320

Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn
 325 330 335

Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe Pro
 340 345 350

Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp Ile
 355 360 365

Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His
 370 375 380

Leu Leu Asp Phe Gln Cys Val Pro Lys Ala Val Ser Asn Leu Thr Glu
 385 390 395 400

Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser Leu Ile Ala Thr
 405 410 415

Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Ala Phe Thr Ala
 420 425 430

Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile Ile Asn Pro Glu
 435 440 445

Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp Phe Gly Phe
 450 455 460

Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
 465 470 475

<210> 6

<211> 496

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: humanized

rabbit CESTP protein

<400> 6

Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys Arg Ile Thr
 1 5 10 15
 Lys Pro Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Val Gln
 20 25 30
 Thr Ala Phe Gln Arg Ala Gly Tyr Pro Asp Val Ser Gly Glu Arg Ala
 35 40 45
 Val Met Leu Leu Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile
 50 55 60
 Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp Ala Lys
 65 70 75 80
 Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr
 85 90 95
 Leu Asn Tyr Ser Tyr Thr Ser Ala Trp Gly Leu Gly Ile Asn Gln Ser
 100 105 110
 Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu
 115 120 125
 Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys Tyr
 130 135 140
 Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro
 145 150 155 160
 Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys
 165 170 175
 Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser Asn
 180 185 190
 Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
 195 200 205
 Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr
 210 215 220
 Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys Asn
 225 230 235 240

Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu Gly
 245 250 255
 Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser
 260 265 270
 Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu Thr
 275 280 285
 Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr Asn
 290 295 300
 Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala
 305 310 315 320
 Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn
 325 330 335
 Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe Pro
 340 345 350
 Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp Ile
 355 360 365
 Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His
 370 375 380
 Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser Ser
 385 390 395 400
 Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
 405 410 415
 Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser Leu
 420 425 430
 Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Ala
 435 440 445
 Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile Ile
 450 455 460
 Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp
 465 470 475 480
 Phe Gly Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
 485 490 495

<210> 7

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: fusion protein
of a tetanus toxoid segment and human CTFP
C-terminus

<400> 7

Cys Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Phe
1 5 10 15

Gly Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
20 25 30